

Figure 1 Interleukin-21

1	GGC	ACG	AGT	GGA	CAC	GGA	TGA	.GGA	.CÇG	CTA	TCC	ACA	GAA	GCT	GGC	CTT	CGC	CGA	GTG	CCT	60
1	Α	R	<u>V</u>	D	T	D	E	D	R	Y	P	Q	K	L	Α	F	A	E	C	<u> </u>	20
					Doi	naiı	ı I											D	oma.	in II	
				•			•			•				•			•			•	
	GTG																				120
21			G		Ι	D	Α	R	т	G	R	E	т	A	A	L	N	S	V	R	40
	Do	omai	in I	Ί																	
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181	ccc	CAC	ACC	ĪĞĞ	GGC	CTT	TGC	CTT	CCA	CAC	CGA	GTT	CAT	CCA	CGT	ccc	CGT	CGG	CTG	CAC	240
61			P					F				F								T	80
																Do	oma:	in :	ΙV		
•																		•			
241	CTG	CGT	GCT	GCC	CCG	TTC	AGT	GTG	ACC	GCC	AAG	GCC	GTG	GGG	CCC	TTA	GAC	TGG	ACA	.CGT	300
81	_ <u>C</u>		L	P	R	s	V														87
L	omai	in 1	v															•			
				•			•							•			•			•	
301	GTG	CTC	:CCC	AGA	GGG	CAC	CCC	CTA	TTT	ATG	TGT	ATT	TAT	TGT	TAT	TTA	TAT	GCC	TCC	CCC	360
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361	770	יאריי	יארר	•		\sim m \sim	· ~~	CC3			CITIC	пуп	~~~	~~~	~~~		•	ъ с тп	V~mem		420
201	AAC	ACI	ACC	CIT	ت	GIC	166	GCA	TTC		GIG	TCT	GGA	ADD	CAG		CCC	ACI	GIT	CIC	420
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421	CTC	ATC	TCC	AGC	CTC	AGT.	- AGT	TGG	GGG	TWG	AAG	GAG	CTC	AGC	ACC	TCT	TCC	AGC	CCT	TAA	480
											_										
481	AGC	TGC	AGA	AAA	GGT	GTC	ACA	.CGĠ	CTG	CCT	GTA	CCT	TGG	YTC	CCT	GTC	CTG	CTC	CCG	GCT	540
										•		•									
541	TCC	CTT	ACC	CTA	TCA	CTG	GCC	TCA	.GGC	CCC	CGC	AGG	CTG	CCT	CTT	CCC	AAC	CIC	CTT	GGA	600
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601	AG1	ACC	CCI	GI-I	TCT	TAA	ACA	ATT.	ATT.	TAA	ف10	TAC	GIG	TAT	TAT	TAA	ACT	GA'I'	GAA	.CAC	660
																	•				
661	ΑΔΑ	ΔΔΔ	ΔΔΔ	AAA	ΔΔΔ	ΑΑΑ	AAA	ΔΔΔ	ΑΑΑ	AAA	ΔΔΔ	ΔΔΔ	ΔΔΔ	222	ΔΔΔ	7	05				

Figure 2A Interleukin-22

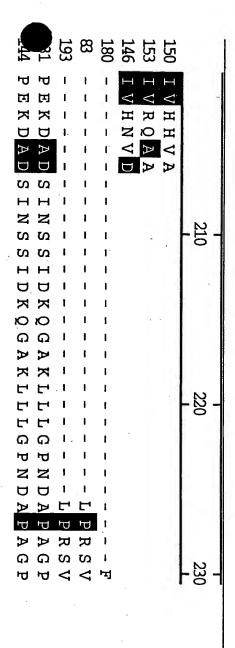
1	GGAA	TTC	GGC.	ACG.	AGC	TCG	TGC	CGT	GCT	CAG	TGC	CTT	CCA	CCA	CAC	GCI	GCA	GCT	GGG	GC	60
1	N	s	A	R	A	R	A	v	L	s	A	F	Н	Н	T	L	Q.	L	G	P	20
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61	CGCG																				120
21	R	E	Q	A	ĸ	N	A	S	C	Р	A	G	G	R	P	А	D	R	R	F	40
121	TCCG	GCC	GCC	CAC	CAA	CCT	GCG	CAG	CGT	GTC	GCC	CTG	GGC	CTA	CAG	LAAT	CIC	CTA	.CGA	CC	180
41	R	P	P	T	N	L	R	s	v	s	P	W	Α	Y	R	I	S	Y	D	_P .	60
									•								D	oma.	in i	T	
181	CGGC	GAG	GTA	ccc	CAG	GTA	CCT	GCC	TGA	AGC	CTA	CTG	CCI	GTG	CCG	GGG	CTG	CCT	GAC	CG	240
61	A_	R	Y	P	R	Y	L	P	E	A	Y	<u>C</u> _	Ļ	С	R	G	C	L	T	G	80
	. Do	omai	n I	•						•			Do	omai	n 1	II					•
241	GGCT	GTT	CGG	CGA	GGA	GGA	CGT	GCG	CTT	CCG	CAG	CGC	ccc	TGT	CTA	CAT	GCC	CAC	CGT	CG	300
81		F		E	E		V		F	R	s	A		V		M		T	V		100
						-	•											Doi	mair	n II	r
301	TCCT	GCG	CCG	CAC	CCC	CGC	· CTG	CGC	:CGG	CGG	CCG	TTC	CGT	CTA	CAC	CGA	JGGC	CTA	CGT	CA	360
101	L												v		т	E	A	Y	v	T	120
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361																					420
121	. 4	Р	V				<u></u>		P	E	P	E	K	D	Α	D	S	I	N	S	140
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421	CCAG	CAT	'CGA	CAA	ACA	GGG	CGC	CAA	GCT	CCI	GCI	GGG	ĆCC	CAA	CGA	CGC	CCC	CGC	TGG	CC	480
141	s	I	D	ĸ	Q	G	A	K	L	L	L	G	P	N	D	A	P	A	G	P	160
481	CCTG	AGG	CCG	GTC	CIG	ccc	CGG	GAG	GTC	TCC	CCC	GCC	CGC	ATC	CCG	AGC	SCGC	CCA	AGC	TG	540
541	GAGC	:CGC	CTG	GAG	GGC	TCG	GTC	:GGC	:GAC	CTC	TGA	AGA	GAG	TGC	ACC	GAG	CAA	ACC	'AAG	TG	600
601	CCGG	AGC	ACC	AGC	GCC	GCC	· TTT	CCA	.TGG	AGA	CTC	GTA	AGC	:AGC	TTC	CTA	MGA	CAC	:GGG	CA	660
661	TCCC	TGG	CTT	GCT	TTT	AGC	TAC	:AAG	CAA	AGCA	'CCC	TGG	CTC	GAA	.GCI	'GA'I	rggc	AAA	.CGA	.cc	720
721	CGGC	ACG	GGC	ATC	CTG	TGT	GCG	GCC	cccc	EATC	GAG	GGI	TTC	GAA	AAC	TTC	CACC	GAG	GCT	CC	780
781	CTGA	GGA	.GCC	TCT	CAG	ATC	GGC	TGC	TGC	GGG	TGC	CAGG	GCC	TGA	CTC	CACC	CCI	.GGG	TGC	TT	840
841	GCCA	AAG	AGA	TAG	GGA	CGC	'ATA	TGC	Alalai	TTA	AAG	CAA	TCT	אַבאַבּ	PAA	יאבי	['AA']	'AAC	TAT	'AG	900

Figure 2B Interleukin-22

901	CGACTATATACCTACTTTTAAAATCAACTGTTTTGAATAGAGGCAGAGCTATTTTATATT	960
961	ATCAAATGAGAGCTACTCTGFTACATTTCTTAACATATAAACATCGTFTFTTACTTCTTC	1020
1021		1080
1081	TGGCCTGGGTCTCTGAATTCAGCCTGTCACCGATGGCTGACTGA	1140
1141	CATCTGACCCACTCTTCCACTGAAGGTCTTCACGGGCCTCCAGGTGGACCAAAGGG	1200
1201		1260
1261		1320
1321	. CCACTGGGGCCAATTTGTGGTTAAGAGGTGGTGAGATAAGAAGTGGAACGTGACATCTTT	1380
1381	GCCAGTTGTCAGAAGAATCCAAGCAGGTATTGGCTTAGTTGTAAGGGCTTTAGGATCAGG	1440
1441	CTGAATATGAGGACAAAGTGGGCCACGTTAGCATCTGCAGAGATCAATCTGGAGGCTTCT	1500
1,501	GTTTCTGCATTCTGCCACGAGAGCTAGGTCCTTGATCTTTTCTTTAGATTGAAAGTCTGT	1560
1561		1620
1621		

Figure 3A

Figure 3B



II-17.aa mII-17.aa vII-17.aa II20.aa II-21.aa

П21FL.аа П-22.аа

II.22ext.aa

Figure 3C

Figure 4
Interleukin-21 Polypeptide Analysis

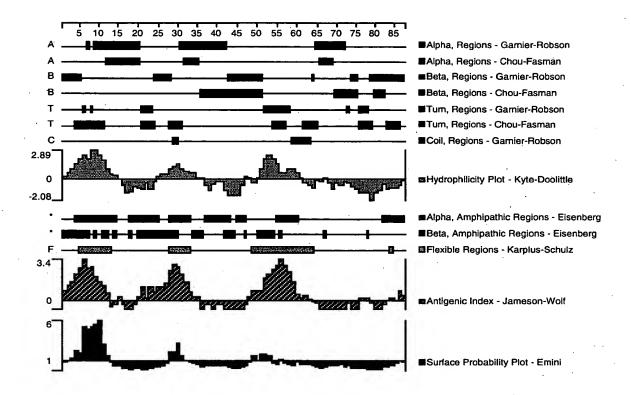


Figure 5
Interleukin-22 Polypeptide Analysis

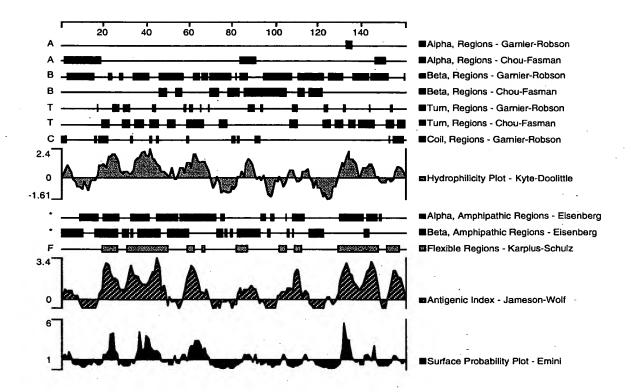


Figure 6A Interleukin-21

										M	T	L	L	P	G	L	L	F
GAC	CTG	GCI	GCA	CAC	ATG	CCT	GGC	CCA	CCA	TGA	ccc	CTC	CCT	CAG	GGG	GCA	ccc	CCAC
T	W	L	H	T	С	L	_ <u>A</u>	Н	Н	D	P	S	L	R	G	H	P	Н
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Н	G	Т	. <u>P</u>					A	_ <u>E</u>	E	L	P	L	G	Q	Α	P	P
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CCI	GCI	GGC	TCG	AGG	TCC	CAA	GTG	GGG	GCA	GGC	TTT	GCC	TGT	'AGC	CCI	GGT	GTC	CAGC
L	L	A	R	G	A	K	W	G	Q	A	L	P					s	S
													D	лна.	LII	/1		
GGA	.GGC	'AGC	'AAG	CCA	CAG	GGG	GAG	GCA	.CGA	GAG	GCC	CTC	'AGC	TAC	GAC	CCA	GTG	CCCG
				Н					E	R	P	s	A	Т	T			P
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GCI	GCG	GCC	:GGA	.GGÃ	GGT	GTI	GGA	GGC	'AGA	CAC	CCA	.CCA	GCG	CTC	CAT	CTC	ACC	CTGG
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P	т	Р	G	Α	F	A	F	н	т	E	F	1	Н	<u>V</u> _				
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CTC	CG1	GCI	GCC	:ccc	TTC	'AGT	GTC	ACC	· GCC	'AAG	GCC	GTC	GGG	ccc	TTP:	GAC	TGG	ACAC
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	T ICA H CCT L GGA Y GTG C CCC P CTG C	T W ICACGO H G CCTGCT L L GGAGGC E A GCTGCG C R COMMAIN GCTGCGI L L CCCCCAC P T	T W L CCACGGTAC H G T CCTGCTGGC L L A GGAGGCAGC E A A GCTGCGGCC L R P ATACCGGGT Y R V GTGCAGAGG C R G Domain II GCTGCTCCA L L Q CCCCACACC P T P	T W L H CACCGTACCCC H G T P CCTGCTGGCTCG L L A R CGAGGCAGCAAG E A A S CCTGCGGGCCGGA ATACCGGGTGGA Y R V D CTGCAGAGGCTG C R G C Comain II CCCCCACACCTGG P T P G CTGCGGGCTGCCCCCC C V L P	TWLHT TCACGGTACCCCACA HGTPH CCTGCTGGCTCGAGG LLARG GGAGGCAGCAAGCCA EAASH GCTGCGGGCCGGAGGA LRPEE ATACCGGGTGGACAC YRVDT DO GTGCAGAGGCTGTAT CRGCI LLQSL CCCCCACACCTGGGGC PTPGA	T W L H T C CCCCCACACCTGGGGCCTC CCCCCACACCTGGGGCCCCCCTTC C V L P R S	TWLHTCL CCACGGTACCCCACACTGCTA HGTPHCY Domain CCTGCTGGCTCGAGGTGCCAA LLARGGAGCCACACGGGGG EAASHRGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	TWLHTCLA CACCGTACCCCACACTGCTACTC CACCGTACCCCACACTGCTACTC HGTPHCYS Domain V CCTGCTGGCTCGAGGTGCCAAGTG LLARRGAAGCCACAGGGGGAG EAASHRGRA GCTGCCGCCCGGAGGAGGTGTTGGA LRPEEVLE ATACCGGTGGACACGGATGAGGA YRVDTDED Domain I GTGCAGAGGCTGTATCGATGCACG CRGCIDAR COMAIN II GCTGCTCCAGAGCCTGCTGGTGCT LLQSLLVL Doma CCCCCACACCTGGGGGCCTTTGCCTT PTPGAFFA CTGCGGGGCTGCCCCCGTTCAGTGTG CVLPRSV	TWLHTCLA H TCACGGTACCCCACACTGCTACTCGGC HGTPHCYSA Domain V CCTGCTGGCTCGAGGTGCCAAGTGGGG LLAARGCCACAGGGGGAGGCA EAAASHRGARGTGTTGGAGGC LRPEEVLEA ATACCGGGTGGACACGGATGAGGACCG YRVDTDEDEDR Domain I CTGCAGAGGCTGTATCGATGCACGGAC CRGCID DART Domain II CCCCCACACTGGGGGCCTTTGCTGCTGCCG LLQSLLVLR Domain CCCCCACACCTGGGGGCCTTTGCCTTCCA PTPGAAFCCCCCTTCCCTTCCACTGTGCTGCCC CVLPRSV CTGCGTGCTGCCCCCCTTCAGTGTGACCC CCVLPRSV CTGCGTGCTGCCCCCCCTTCAGTGTGACCC CCVLPRSV CTGCGTGCTGCCCCCCCTTCAGTGTGACCC CCVLPRSV CTGCGTGCTGCCCCCCCTTCAGTGTGACCC CCVLPRSV CTGCGTGCTGCCCCCCCTTCAGTGTGACCC CCCCCCCCCC	TWLHTCLAHH CACCGTACCCCACACTGCTACTCGGCTGA HGTPHCYSA Domain V CCTGCTGGCTCGAGGTGCCAAGTGGGGGCA LLARRGAK KWGQ GGAGGCAGCAAGCCACAGGGGGAGGCACGA EAASHRGRAGCACAGGGGGGAGGCACGA EAASHRGRAGCACAGGGGGGAGGCACGA LRPEEVLEAD ATACCGGTGGACACGGATGAGGACCGCTA YRVDTDEDRY Domain I GTGCAGAGGGTGTATCGATGCACGGACGGG CRGCI DARTG MATACCGGTGCACAGGGCTGTTTGGAGGCACGGG CRGCI DARTG MATACCGGTTGACACGGATGAGGACCGCTA YRVDTDEDRY Domain II GCTGCTCCAGAGGCTGTTATCGATGCACGGACGGG CRGCI LVLRR Domain III CCCCCCACACCTGGGGCCTTTGCCTTCCACACC PTPGAFFAFAFAFATT CTGCGTGCTCCACACCGGGCCCCCCCCCCCCCCCC	GACCTGGCTGCACACATGCCTGGCCCACCATGA T W L H T C L A H H D TCACGGTTACCCCACACTGCTACTCGGCTGAGGA H G T P H C Y S A E E Domain V CCTGCTGGCTCGAGGTGCCAAGTGGGGCAGGC L L A R G A K W G Q A GGAGGCAGCAAGCCACAGGGGGAGGCACGAGAG E A A S H R G R H E R GCTGCGGCCGGAGGAGGTGTTGGAGGCAGACAC L R P E E V L E A D T ATACCGGTGGACACGGATGAGGACCGCTATCC Y R V D T D E D R Y P Domain I GTGCAGAGGCTGTATCGATGCACGGACGGCCG C R G C I D A R T G R Domain II GCTGCTCCAGAGCCTGCTGCTGCTGCGCCGCCG L L Q S L L V L R R R Domain III CCCCCACACCTGGGGCCCTTTGCCTTCCACACCGA P T P G A F A F H T E CTGCGTGCTGCCCCCCGTTCAGTGTGACCGCCAAGC C V L P R S V	GACCTGGCTGCACACATGCCTGGCCCACCATGACCC T W L H T C L A H H D P TCACGGTACCCCACACTGCTACTCGGCTGAGGAACT H G T P H C Y S A E E L Domain V CCTGCTGGCTGGAGGTGCCAAGTGGGGGCAGGCTTT L L A R G A K W G Q A L GGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCC E A A S H R G R H E R P GCTGCGGCCGGAGGAGGTGTTGGAGGACGACACCCA L R P E E V L E A D T H ATACCGGGTGGACACGGATGAGGACCGCTATCCACA Y R V D T D E D R Y P Q Domain I GTGCAGAGGCTGTATCGATGCACGGACGGCCGCGA C R G C I D A R T G R E Comain II GCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGCCGCC L L Q S L L V L R R R P Domain III CCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTT P T P G A F A F H T E F CTGCGTGCTCCCCCCGTTCAGTGTGACCGCCAAGGCC C V L P R S V	GACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTC T W L H T C L A H H D P S TCACGGTACCCCACACTGCTACTCGGCTGAGGAACTGCC H G T P H C Y S A E E L P Domain V CCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCC L L A R G A K W G Q A L P GGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTC E A A S H R G R H E R P S GCTGCGGCCGGAGGAGGTGTTGGAGGACACCCACCA L R P E E V L E A D T H Q ATACCGGGTGGACACGGATGAGGACCCCTATCCACAGAA Y R V D T D E D R Y P Q K Domain I GTGCAGAGGCTGTATCGATGCACGGACGGCCGGAGAC C R G C I D A R T G R E T Nomain II GCTCCTCCAGAGCCTGCTGGTGCTGCGCCCCCGGCCCTC L L Q S L L V L R R R P C Domain III CCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCAT P T P G A F A F H T E F I CTGCGTGCTGCTGCCCCCCCGGCCCTTCCCCCCCCCC	GACCTGCTGCACACATGCCTGCCCACCATGACCCCTCCTT TWLHTCLA H H D P S L PRACGGTACCCCACACTGCTACTCGGCTGAGGAACTGCCCCT H G T P H C Y S A E E L P L Domain V CCTGCTGGCTGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGT L A R G A K W G Q A L P V DOMAIN V CGTGCTGGCTGAGGTGCCAAGTGGGGGAGGCCCTCAGC E A A S H R G R H E R P S A CGTGCCGCCCGGAGGAGGCTTTGGAGGAGGCCCTCAGC L R P E E V L E A D T H Q R ATACCGGGTGGACACGGATGAGGACCGCTATCCACAGAAGCT Y R V D T D E D R Y P Q K L Domain I CGTGCAGAGGCTGTATCGATGAGGACGGCCGCGAGACACC L R G C I D A R T G R E T A COMMAIN II CCCCCACACCTGGGGCCTTTGCCTTCCACACAGAGGTTCATCCAC P T P G A F A F H T E F I H CCTGCGTGCTGCCCCCGGTTCAGTGTGACCGCCAAGGCCGTGCCCCCCCC	GACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCT	GACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCT	GACCTGCTCCACACATCCCTCGCCCACCATGACCCCTCCCT	GACCTGCCTCCACACACTCCCTGGCCCACCATGACCCCTCCCT

Figure 6B Interleukin-21

781	TCCTCATCTCCAGCCTCAGTAGTTGGGGGGTWGAAGGAGCTCAGCACCTCTTCCAGCCCTT	840
841	AAAGCTGCAGAAAAGGTGTCACACGGCTGCCTGTACCTTGGYTCCCTGTCCTGCTCCCGG	900
901	CTTCCCTTACCCTATCACTGGCCTCAGGCCCCCGCAGGCTGCCTCTTCCCAACCTCCTTG	960
961	GAAGTACCCCTGTTTCTTAAACAATTATTTAAGTGTACGTGTATTATTAAACTGATGAAC	1020
021		

Figure 7
Interleukin-21 Polypeptide Analysis

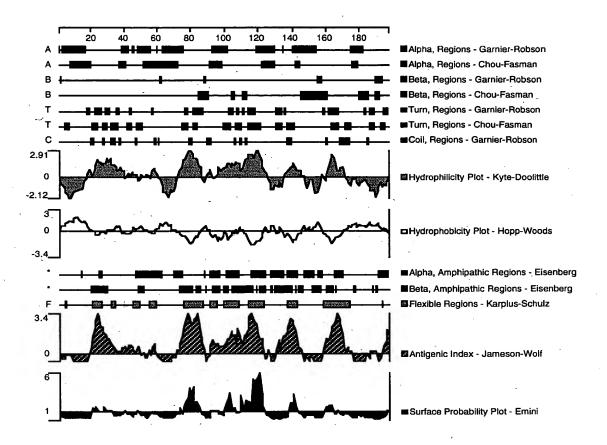


Figure 8 Interleukin-22

1	GG	CTG	CGC	GGA	CCG	GCC	GGA	GGA	GCT	ACI	'GGA	.GCA	GCT	GTA	.CGG	GCG	CCI	'GGC	GGC	CGGC	60
1	G	С	Α	D	R	P	E	\mathbf{E}	L	L	E	Q	L	Y	G	R	L	A	Α	G	20
																			CD-1	π	
			•																#	٠.	
61	GT	GCT	CAG	TGC	CTI	CCA	CCA	CAC	GCT	GCA	GCÍ	GGG	GCC	GCG	TGA	GCA	GGC	:GCG	CAA	CGCG	120
21	V_	Ĺ	s	Α	F	H	н	т	L	Q	L	G	P	R	E	Q	Α	R	N	A	40
	CI)-VI														~			*		
		-	-				_							_						_	
121	AG	CTG	ccc	ĠĠĊ	AGG	GGG	CAG	GCC	CGC	CGA	CCG	CCG	СТТ	CCG	GCC	GCC	CAC	ĊAA	CCT	GCGC	180
41																				R	60
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181	AG	ССТ	CTC	بردر. ب	CALC:	ccc	מידיייייי	CAG	:AAT	УТРУ	אידיי	CGA	ccc	'GGC	'GAG	ርጥል		ዮልና	СТА	CCTG	240
61																		R			80
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241	~	מבית	ACC	מינייטי	CITC	זייירי	י בעונבע	2000	ccc	دربارت	·	יכאר	rcc	י. י	Y2TVT	Y	מבריי	CCA	CCA	CGTG	300
81			- 0															E			100
01	-	-	^	-	<u>_</u>		CD-				ם	-	G	ш	F	G		E		٧	100
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301	~		~~		~~	~~~	****************	vyn z	CAM	~~~	•	·~~	V-CT		~~~	~~~	-		~~~	CTGC	360
101																		P			120
101	К	F	K	5	A	Ρ.	٧	I	M	P	1	<u>v</u>					.T.		A	C	120
														CI	D-II	LI					
261		~~~						~~~	.~~	~~~											400
							-				-									CTGC	420
121	Α	G	G	R ·	S	V	Y	T	E	A	Y	V	т	I.	Р.				T	<u> </u>	140
				•												•	CD	IV			
				•			-				•	#		•				•		•	
																'CGA				CGCC	480
141	<u>v</u>	P	E	P	E	K	D	A	D	S	Ι	N	s	S	I	D	K	Q	G	A	160
	D-1	V										-									
				•										•							
481	AA	GCT	CCI	CT	GGC	CCC	CAA	CGA	CGC	:GCC	CGC	TGG	CCC	CTC	A	522					
161	K	L	L	L	G	P	N	D.	Α	P	Α	G	P			174					

Figure 9
Interleukin-22 Polypeptide Analysis

